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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/566,201	01/27/2006	Artur Pfitzner	MBP-033XX	8282
207 7590 06/21/2007 WEINGARTEN, SCHURGIN, GAGNEBIN & LEOVICI LLP TEN POST OFFICE SQUARE BOSTON, MA 02109			EXAMINER BAGGOT, BRENDAN O	
			ART UNIT 1638	PAPER NUMBER
			MAIL DATE 06/21/2007	DELIVERY MODE PAPER

**Please find below and/or attached an Office communication concerning this application or proceeding.**

The time period for reply, if any, is set in the attached communication.

<b>Office Action Summary</b>	<b>Application No.</b> 10/566,201	<b>Applicant(s)</b> PFITZNER ET AL.	
	<b>Examiner</b> Brendan O. Baggot	<b>Art Unit</b> 1638	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

#### Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

#### Status

- 1) ☒ Responsive to communication(s) filed on 16 March 2007.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

#### Disposition of Claims

- 4) ☒ Claim(s) 1-16 and 18-33 is/are pending in the application.
- 4a) Of the above claim(s) 15, 16, 18, 19 and 29-33 is/are withdrawn from consideration.
- 5) ☐ Claim(s) \_\_\_\_\_ is/are allowed.
- 6) ☒ Claim(s) 1-14 and 20-28 is/are rejected.
- 7) ☐ Claim(s) \_\_\_\_\_ is/are objected to.
- 8) ☐ Claim(s) \_\_\_\_\_ are subject to restriction and/or election requirement.

#### Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☒ The drawing(s) filed on 27 January 2006 is/are: a) ☒ accepted or b) ☐ objected to by the Examiner.  
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).  
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

#### Priority under 35 U.S.C. § 119

- 12) ☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☒ All b) ☐ Some \* c) ☐ None of:
- ☐ Certified copies of the priority documents have been received.
  - ☐ Certified copies of the priority documents have been received in Application No. \_\_\_\_\_.
  - ☒ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

\* See the attached detailed Office action for a list of the certified copies not received.

#### Attachment(s)

- |  |   |
|--|---|
| 1) <input checked="" type="checkbox"/> Notice of References Cited (PTO-892)            | 4) <input type="checkbox"/> Interview Summary (PTO-413)           |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948)   | Paper No(s)/Mail Date. _____                                      |
| 3) <input checked="" type="checkbox"/> Information Disclosure Statement(s) (PTO/SB/08) | 5) <input type="checkbox"/> Notice of Informal Patent Application |
| Paper No(s)/Mail Date <u>1/27/06; 3/26/06</u>  | 6) <input type="checkbox"/> Other: _____                          |

## **DETAILED ACTION**

### ***Restriction / Election***

1. Applicant's election with traverse of Applicant elects Group I, claims 1-14, 20-28, and SEQ ID NO: 1 only, in the reply filed on 3/16/07 is acknowledged. The traversal is on the ground(s) that "...not seen as ...undue burden ....". This is not found persuasive because while a search of the prior art for one group may overlap with that of another group, they are not co-extensive of each other and thus would represent undue burden on Office resources.

2. Claims 15-16, 18-19, 29-33 and sequences other than SEQ ID NO: 1 are withdrawn from further consideration pursuant to 37 CFR 1.142(b), as being drawn to a nonelected inventions, there being no allowable generic or linking claim. Applicant timely traversed the restriction (election) requirement in the reply filed on 3/16/07.

3. Claims 1-14, 20-28 are examined in the instant application.

4. The requirement is deemed proper and is therefore made FINAL.

### ***Sequence Listing***

5. Applicant's computer readable format sequence listing has been entered.

### ***Drawings***

6. The drawings are acceptable for examination.

### ***Claim Objections***

Art Unit: 1638

7. Claim 1 is objected to because of the following informalities: the claim recites non-elected SEQ ID NOs. Appropriate correction is required.

8. Claims 9, 21 are objected to because of the following informalities: the claim recites the "... host organism ... is ... a plant cell." Plant cells are not organisms. Appropriate correction is required.

9. Claim 1 is objected to because of the following informalities: the claim recites an improper Markush group drawn to 2 members of a genus and a separate genus. Appropriate correction is required.

***Claim Rejections - 35 U.S.C. §112, second paragraph***

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

10. Claims 1-14 and 20-28 rejected under 35 U.S.C. §112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which the applicant regards as the invention.

11. In Claims 1-14 and 20-28, it is unclear what is being retained in the derived product.

***Claim Rejections - 35 USC § 112, 1<sup>st</sup>, paragraph, written description***

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the

Art Unit: 1638

art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

A description of a genus of cDNAs may be achieved by means of a recitation of a *representative number* of cDNAs, defined by nucleotide sequence, falling within the scope of the genus *or* of a recitation of *structural features* common to the members of the genus, which features constitute a substantial portion of the genus. *University of California v. Eli Lilly and Co.*, 43 USPQ2d 1398 (Fed. Cir. 1997). (emphasis added).

See also *Fiddes v. Baird*, 30 USPQ2d 1481 (Bd. Pat. App. & Int. 1993); *In re Curtis*, 69 USPQ2d 1274, 1282 (Fed. Cir. 2004); *Fiers v. Revel*, 25 USPQ2d 1601 (Fed. Cir. 1993); *Amgen Inc. v. Chugai Pharmaceutical.*, 18 USPQ2d 1016 (Fed. Cir. 1991).

12. Claims 1-14 and 20-28 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claims are broadly drawn to an inducible promoter, SEQ ID NO: 1 (NIMIN-1 promoter), biologically active derivatives of SEQ ID NO: 1 of any length and sequence from any source, "chemicals" and "organic compounds" capable of inducing SEQ ID NO: 1, and undescribed heterologous nucleic acid sequences encoding wild-type or mutant NIMIN-1 promoters. Said sequences include genes encoding promoters from any source (Claim 1-14, 20-28), as well as any sequence from any source encoding any promoter which has any biological activity of any kind, including irreversible self-excision from the genome.

In contrast, Applicant has only described SEQ ID NO: 1(sequence listing), GUS expression data with NIMIN-1 (SEQ ID NO: 1)-GUS fusions (Examples 2-3), and transgenic tobacco plants containing SEQ ID NO: 1-GUS constructs(Examples 2-3).

Applicant does not describe biologically active derivatives of SEQ ID NO: 1 of any length and sequence from any source, any "chemicals" (e.g., mercury or water) or any "organic compounds" (e.g., cyanide or glyphosate) capable of inducing SEQ ID NO: 1, and undescribed heterologous nucleic acid sequences encoding wild-type or mutant SEQ ID NO: 1 promoters. Said sequences include genes encoding promoters from any source (Claim 1-14, 20-28), as well as any sequence from any source encoding any promoter with any or no promoter activity.

Applicant has not described the structure or any other relevant characteristics for all nucleic acid sequences encoding biologically active derivatives of NIMIN-1 promoters, or a representative number of same and a literature review does not indicate that they are well known to one of skilled in the art. Applicant has only described nucleic acid sequences encoding SEQ ID NO: 1 from *Arabidopsis*.

Applicant fails to describe a representative number of biologically active derivatives of SEQ ID NO: 1, or chemicals or organic compounds capable of inducing said biologically active derivatives. Applicant only describes SEQ ID NO: 1. Furthermore, Applicant fails to describe structural features common to members of the claimed genus of biologically active derivatives of SEQ ID NO: 1. Hence, Applicant fails to meet either prong of the two-prong test set forth by *Eli Lilly*. Furthermore, given the lack of description of the necessary elements essential for NIMIN-1 promoter

activity, it remains unclear what features identify NIMIN-1 promoters. Since the genus of NIMIN-1 promoters or the genus of biologically active fragments thereof has not been described by either specific structural features or a representative number of species, the specification fails to provide an adequate written description to support the breadth of the claims.

The Federal Circuit has clarified the application of the written description requirement. The court stated that a written description of an invention "requires a precise definition, such as by structure, formula, [or] chemical name, of the claimed subject matter sufficient to distinguish it from other materials." *University of California v. Eli Lilly and Co.*, 119 F.3d 1559, 1568; 43 USPQ2d 1398, 1406 (Fed. Cir. 1997); See also *Fiddes v. Baird*, 30 USPQ2d 1481 (Bd. Pat. App. & Int. 1993). The court also concluded that "naming a type of material generally known to exist, in the absence of knowledge as to what that material consists of, is not a description of that material." *Eli Lilly*. Further, the court held that to adequately describe a claimed genus, Patent Owner must describe a representative number of the species of the claimed genus, and that one of skill in the art should be able to "visualize or recognize the identity of the members of the genus." *Id.*

Finally, the court held:

A description of a genus of cDNAs may be achieved by means of a recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or a recitation of structural features common to members of the genus, which features constitute a substantial portion of the genus. *Id.*

See also MPEP Section 2163, page 174 of Chapter 2100 of the August 2005 version, column 1, bottom paragraph, where it is taught that

[T]he claimed invention as a whole may not be adequately described where an invention is described solely in terms of a method of its making coupled with its function and there is no described or art-recognized correlation or relationship between the structure of the invention and its function. A biomolecule sequence described only by a functional characteristic, without any known or disclosed correlation between that function and the structure of the sequence, normally is not a sufficient identifying characteristic for written description purposes, even when accompanied by a method of obtaining the claimed sequence.

See also *Amgen Inc. v. Chugai Pharmaceutical Co. Ltd.*, 18 USPQ 2d 1016 at 1021, (Fed. Cir. 1991) where it is taught that a gene is not reduced to practice until the inventor can define it by "its physical or chemical properties" (e.g. a DNA sequence).

Given the claim breadth and lack of guidance as discussed above, the specification fails to provide an adequate written description of the genus of sequences as broadly claimed. Given the lack of written description of the claimed genus of sequences, any method of using them, such as transforming plant cells and plants therewith, and the resultant products including the claimed transformed plant cells and plants containing the genus of sequences, would also be inadequately described. Accordingly, one skilled in the art would not have recognized Applicant to have been in possession of the claimed invention at the time of filing. See The Written Description Requirement guidelines published in Federal Register/ Vol. 66, No. 4/ Friday January 5, 2001/ Notices: pp. 1099-1111.



***Claim Rejections - 35 U.S.C. §112, first paragraph, enablement***

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

13. Claims 1-14 and 20-28 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for SEQ ID NO: 1, does not reasonably provide enablement for biologically active derivatives of SEQ ID NO: 1. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in scope with these claims.

The *Wands* court set forth the enablement balancing test:

Factors to be considered in determining whether a disclosure meets the enablement requirement of 35 USC 112, first paragraph, have been described by the court in *In re Wands*, 858 F.2d 731, 8 USPQ2d 1400, 1404 (Fed. Cir. 1988). *Wands* states at page 1404, "Factors to be considered in determining whether a disclosure would require undue experimentation have been summarized by the board in *Ex parte Forman*. They include (1) the quantity of experimentation necessary, (2) the amount of direction or guidance presented, (3) the presence or absence of working examples, (4) the nature of the invention, (5) the state of the prior art, (6) the relative skill of those in the art, (7) the predictability or unpredictability of the art, and (8) the breadth of the 'claims.'"

M.P.E.P. § 2164.01(a); *See also Ex Parte Forman* 230 USPQ 546, 547 (BdPatAppInt 1986); *See also Enzo Biochem, Inc., v. Calgene, Inc.*, 188 F.3d 1362, 52 USPQ2d 1129 (Fed. Cir. 1999).

The claims are broadly drawn to an inducible promoter, SEQ ID NO: 1 (NIMIN-1 promoter), biologically active derivatives of SEQ ID NO: 1 of any length and sequence

from any source, "chemicals" and "organic compounds" capable of inducing SEQ ID NO: 1, and undescribed heterologous nucleic acid sequences encoding wild-type or mutant NIMIN-1 promoters. Said sequences include genes encoding promoters from any source (Claim 1-14, 20-28), as well as any sequence from any source encoding any promoter which has any biological activity of any kind, including irreversible self-excision from the genome:

In contrast, Applicant has only teaches SEQ ID NO: 1(sequence listing), GUS expression data with NIMIN-19 (SEQ ID NO: 1)-GUS fusions (Examples 2-3), and transgenic plants containing SEQ ID NO: 1-GUS constructs(Examples 2-3).

Applicant do not teach biologically active derivatives of SEQ ID NO: 1 of any length and sequence from any source, "chemicals" (e.g., mercury or water) or "organic compounds" (e.g., cyanide or glyphosate) capable of inducing SEQ ID NO: 1, and undescribed heterologous nucleic acid sequences encoding wild-type or mutant SEQ ID NO: 1 promoters. Said sequences include genes encoding promoters from any source (Claim 1-14, 20-28), as well as any sequence from any source encoding any promoter which somehow "modulates" expression or activity of a gene of interest.

*The Breadth Of The Claims*

See above.

*The Unpredictability of the Art and the State of the Prior Art*

The state-of-the-art is such that one of skill in the art cannot predict which "biologically active derivatives of SEQ ID NO: 1" will work *a priori*. Reviews by Kim,

Hannenhalli, Maiti, and Doelling detail a variety of problems seen in promoter identification and modification.

The state of the prior art, as exemplified by Kim et al (Plant Molecular Biology, vol. 24, pp. 105-117, 1994)) teaches the extreme sensitivity of promoter regions to single base pair changes, the absolute requirement for as few as 3 to 6 nucleotides for promoter function, and the failure of a promoter to function either constitutively or specifically when lacking oligonucleotide regions approximately 100 bp upstream of the transcription start site (page 106, paragraph bridging the columns; paragraph bridging pages 107 and 108; page 110, paragraph bridging the columns). In addition, the claimed nucleic acid sequence that is a biologically active derivatives of SEQ ID NO: 1 would comprise non- functional transcriptional and translational elements, i.e. modifications of CAAT, TATA and the ATG codon, required for proper initiation of these cellular activities, known in the prior art; as well as highly conserved promoter regions rendered inactive by modifications. In addition, Applicant has not shown that any biologically active derivative of SEQ ID NO: 1 can also have the desired promoter activity.

A recent review by Hannenhalli (2001) Bioinformatics 17: S90-S96) teaches that prediction of eukaryotic promoters has been one of the most elusive problems despite considerable effort devoted to the study. (See the abstract at least). In the instant case of a promoter, Hannenhalli's review teaches a 50% failure in the sensitivity of promoter detection (p. S90, last full sentence).

Twenty base-pair long regions of a DNA fragment that has promoter activity cannot predictably be assumed to also have promoter activity. Deletion analysis of various promoters have shown that even DNA segments from the portion of a promoter region containing sequence elements thought to be most important (e.g., the TATA-box) need to be longer than 20 basepairs. Maiti et al, in studies on a figwort mosaic virus promoter, found that the smallest portion upstream of the transcriptional start site that would support transcription was 198 basepairs long; segments of 73 and 37 basepairs did not work (1997, Transgen. Res., 6:143-156, see Fig. 4). Doelling et al found that the minimal rRNA promoter of *Arabidopsis thaliana* is at least 33 nucleotides long (1995, Plant J. 8:683-692, see Fig. 1).

#### *Guidance in the Specification*

See above. The specification, while suggesting the use of the SEQ ID NO: 1, did not provide significant guidance on how to overcome art recognized problems in achieving expression of promoter smaller "biologically active derivatives of SEQ ID NO: 1" of DNA, including single base pair polynucleotide promoters while still retaining activity.

In addition, since the working examples disclosed in the specification are limited to unmodified SEQ ID NO: 1, the chemically inducible activity of sequences cannot be extrapolated to any derivatives thereof, absent specific guidance. While Applicant is not required to exemplify each and every claimed embodiment, specific guidance as to

which region of the disclosed sequences can be modified, truncated so that the s  
chemically inducible activity promoter activity is retained is required.

The specification has no working examples of sequences other than SEQ ID NO:  
1 and no working examples of any "biologically active derivatives of SEQ ID NO: 1".

Without sufficient guidance, identification of NIMIN-1 promoters is unpredictable  
and without guidance on how to overcome the problems seen in determining *a priori*  
which sequences will have NIMIN-1 promoter activity transgenic plants, it is  
unpredictable and the experimentation left to those skilled in the art is unnecessarily  
and improperly extensive and undue.

Therefore, given the breadth of the claims; the lack of guidance and working  
examples; the unpredictability in the art; and the state-of-the-art as discussed above,  
undue trial and error experimentation would be required to practice the claimed  
invention, and therefore the invention is not enabled throughout the broad scope of the  
claims.

### ***Claim Rejections - 35 U.S.C. §102***

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that  
form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(b) the invention was patented or described in a printed publication in this or a foreign country or in public  
use or on sale in this country, more than one year prior to the date of application for patent in the United  
States.

35 U.S.C. §102.

14. Claims 1-5 are rejected under 35 U.S.C. 102(b) as being anticipated by Sato, S., (2000) Structural analysis of *Arabidopsis thaliana* chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty P1 and TAC clones. J. DNA Res. 7 (2), 131-135. (See Appendix A). Sato discloses a recombinant nucleic acid containing at least a first nucleotide sequence operably linked to at least a second nucleotide sequence containing a transgene to be expressed, wherein the first nucleotide sequence contains a regulatory sequence selected from the group consisting of SEQ-ID-No. I, and a biologically active derivative thereof, wherein the regulatory sequence is a promoter sequence selectively inducible by chemicals, wherein the chemicals are selected from the group consisting of organic compounds, wherein the organic compounds are selected from the group consisting of phenolic compounds, thiamine, benzoic acid, isonicotinic acid (INA), and derivatives thereof, wherein the phenolic compound is salicylic acid or a structural or functional derivative thereof, wherein the expression/transcription of said nucleotide sequence results in a detectable signal, a vector containing the recombinant nucleic acid according, and a bacterial host cell. (*Id.* @ p. 131, left column, 1<sup>st</sup> paragraph). Because Sato discloses cloning bugs with cloning vectors, Sato discloses the limitations of the claimed invention. Thus, the reference discloses all the limitations of the Claimed invention.

15. Claims 1-5 are rejected under 35 U.S.C. 102(b) as being anticipated by Federspiel et al, (Database EMBL, 7 February 2000, Federspiel: *Arabidopsis thaliana* chromosome I BAG T14P4 genomic sequence, complete sequence. Database accession no. AC022521, See Appendix B) discloses a recombinant nucleic acid

containing at least a first nucleotide sequence operably linked to at least a second nucleotide sequence containing a transgene to be expressed, wherein the first nucleotide sequence contains a regulatory sequence selected from the group consisting of SEQ-ID-No. I, and a biologically active derivative thereof, wherein the regulatory sequence is a promoter sequence selectively inducible by chemicals, wherein the chemicals are selected from the group consisting of organic compounds, wherein the organic compounds are selected from the group consisting of phenolic compounds, thiamine, benzoic acid, isonicotinic acid (INA), and derivatives thereof, wherein the phenolic compound is salicylic acid or a structural or functional derivative thereof. Thus, the reference discloses all the limitations of the Claimed invention.

16. Claims 1-14 and 20-28 are rejected under 35 U.S.C. 102(b) as being anticipated by Lebel et al discloses chemically inducible genes inducible by salicylic acid and uses thereof (Lebel, et al WO 98 03536 A1/1998, SEQ ID NO: 1, page 5, paragraph 2, lines 2-6).

Lebel discloses a recombinant nucleic acid containing at least a first nucleotide sequence operably linked (See claim 5) to at least a second nucleotide sequence containing a transgene to be expressed, wherein the first nucleotide sequence contains a regulatory sequence selected from the group consisting of a biologically active derivative SEQ-ID-No. I (See sequence listing), wherein the regulatory sequence is a promoter sequence selectively inducible by chemicals (See claim 1(a-c)), wherein the chemicals are selected from the group consisting of organic compounds (See page 2, line 9, 21-25), wherein the organic compounds are selected from the group consisting of

Art Unit: 1638

phenolic compounds, thiamine, benzoic acid, isonicotinic acid (INA), and derivatives thereof (See abstract, page 2, line 9, 21-25, page 10, line 6-26), wherein the phenolic compound is salicylic acid (See abstract) or a structural or functional derivative thereof (See abstract, page 2, lines 9, 21-25; page 10, lines 6-26), wherein the expression/transcription of said nucleotide sequence results in a detectable signal (claim 8; page 9, lines 18-26), a vector (claim 10) containing the recombinant nucleic acid, a host organism (claim 10), a bacterial or plant cell (claim 10), a transgenic plant wherein the recombinant nucleic acid is stably integrated into the genetic material (claim 10), wherein the transgene contained in the second nucleotide sequence is transiently expressed (See page 13, lines 9-18; note that the expression is measured in minutes), and wherein the expression of the transgene contained in the second nucleotide sequence is selectively induced upon treatment with chemicals (See page 14, lines 20-25).

Biologically active fragment is interpreted to encompass a single nucleotide base pair.

Thus the reference anticipates the claimed invention.

17. No Claim is allowed.

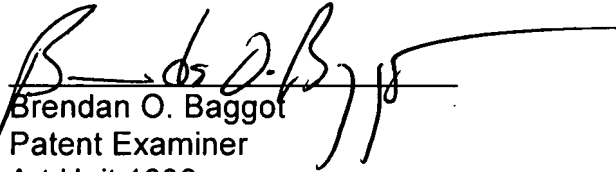
Any inquiry concerning this communication or earlier communications from the examiner should be directed to Brendan O. Baggot whose telephone number is 571/272-5265. The examiner can normally be reached on Monday - Friday.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Anne Marie Grunberg can be reached on 571/272-0975. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

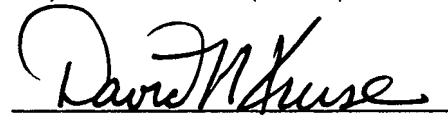


Art Unit: 1638

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Brendan O. Baggot  
Patent Examiner  
Art Unit 1638



David H. Kruse, PhD  
Primary Examiner  
Art Unit 1638

**DAVID H. KRUSE, PH.D.**  
**PRIMARY EXAMINER**

bob

## APPENDIX A

SCORE Search Results Details for Application 10566201 and Search Result us-10-566-201-2.rge.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10566201 and Search Result us-10-566-201-2.rge.

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OM nucleic - nucleic search, using sw model

Run on: September 28, 2006, 01:51:24 ; Search time 11528 Seconds  
(without alignments)  
6800.793 Million cell updates/sec

Title: US-10-566-201-2  
Perfect score: 1226  
Sequence: 1 gatctctatgtatataaaaa.....ttgactaagcttaaacgacg 1226

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_env:\*  
2: gb\_pat:\*  
3: gb\_ph:\*  
4: gb\_pl:\*  
5: gb\_pr:\*  
6: gb\_ro:\*  
7: gb\_sts:\*  
8: gb\_sy:\*  
9: gb\_un:\*  
10: gb\_vi:\*  
11: gb\_ov:\*  
12: gb\_htg:\*

Art Unit: 1638

13: gb\_in:\*  
 14: gb\_om:\*  
 15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	% Query					Description
	No.	Score	Match	Length	ID	
	1	1226	100.0	1226	2	CS007929 Sequence
	2	1226	100.0	1226	2	CS025770 Sequence
c	3	1226	100.0	83650	4	AB023041 Arabidops
	4	941	76.8	92620	4	AB026636 Arabidops
	5	837	68.3	1700	2	AR488147 Sequence
c	6	797.8	65.1	83646	4	AB005248 Arabidops
	7	797.6	65.1	94487	4	AC012394 Arabidops
c	8	797.6	65.1	100806	4	AC015450 Arabidops
c	9	739.2	60.3	104386	4	ATT32A17 Arabidops
c	10	739.2	60.3	179771	4	ATCHRIV25 Arabidops
	11	691	56.4	95519	4	AF071527 Arabidops
c	12	691	56.4	116448	4	AC005142 Arabidops
c	13	691	56.4	159629	4	ATCHRIV9 Arabidops
c	14	553.2	45.1	95190	4	AC007203 Arabidops
	15	231.8	18.9	105223	4	AC007399 Arabidops
c	16	114.6	9.3	349980	2	AX344555 Sequence
	17	112	9.1	175544	12	AC117342 Rattus no
	18	111.2	9.1	4660	2	CS083843 Sequence
	19	111.2	9.1	90550	5	AL592166 Human DNA
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c	21	108.8	8.9	183181	4	AL161507 Arabidops
	22	107.6	8.8	1524	2	CS083838 Sequence
	23	107.6	8.8	212999	12	AC151201 Bos tauru
c	24	107.4	8.8	170627	12	AC125567 Rattus no
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	33	104.2	8.5	241619	12	AC167751 Bos tauru
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c	37	100.8	8.2	169510	12	CR855864 Danio rer
c	38	100.8	8.2	178273	12	AC005308 Plasmodiu
	39	100.8	8.2	250531	13	AE014845 Plasmodiu
	40	100.6	8.2	155942	12	AC136691 Homo sapi
	41	100.6	8.2	161765	5	AC113190 Homo sapi
	42	100.6	8.2	176479	12	AC135631 Homo sapi
c	43	100.2	8.2	192265	5	CNS018P3 Human chr
	44	100	8.2	154604	11	AL954739 Zebrafish

Art Unit: 1638

45 99.8 8.1 67970 13 PFMAL1P3

AL031746 Plasmodiu

## ALIGNMENTS

## RESULT 3

AB023041/c

LOCUS AB023041 83650 bp DNA linear PLN 14-FEB-2004

DEFINITION Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPE11.

ACCESSION AB023041 BA000014

VERSION AB023041.1 GI:4220640

KEYWORDS .

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

## REFERENCE 1

AUTHORS Sato, S., Nakamura, Y., Kaneko, T., Katoh, T., Asamizu, E. and Tabata, S.

TITLE Structural analysis of Arabidopsis thaliana chromosome 3. I.  
Sequence features of the regions of 4,504,864 bp covered by sixty  
P1 and TAC clones

JOURNAL DNA Res. 7 (2), 131-135 (2000)

PUBMED 10819329

## REFERENCE 2 (bases 1 to 83650)

AUTHORS Sato, S., Nakamura, Y., Kaneko, T., Kato, T., Asamizu, E. and Tabata, S.

TITLE Direct Submission

JOURNAL Submitted (01-FEB-1999) Yasukazu Nakamura, Kazusa DNA Research  
Institute, Department of Plant Gene Research; 1532-3, Yana,  
Kisarazu, Chiba 292-0812, Japan (E-mail: ynakamu@kazusa.or.jp,  
Tel: 81-438-52-3935, Fax: 81-438-52-3934)

## COMMENT

Address for correspondence: kaos@kazusa.or.jp  
For the latest information on annotation of this clone, please see  
[http://www.kazusa.or.jp/kaos/cgi-bin/agd\\_graph.cgi?c=MPE11](http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MPE11)  
Genes with similarity to proteins in the databases are described in  
'product' or 'note' qualifiers. Genes that have no significant  
protein similarity are described as 'unknown protein'.  
The software programs used to predict genes include: Grail  
(Informatics Group, Oak Ridge National Laboratory,  
<http://compbio.ornl.gov/Grail-1.3/>),  
GENSCAN (Chris Burge, MIT, <http://CCR-081.mit.edu/GENSCAN.html>),  
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of  
Denmark, <http://www.cbs.dtu.dk/services/NetGene2/>) and  
SplicePredictor (Volker Brendel, Stanford University,  
<http://gremlin1.zool.iastate.edu/cgi-bin/sp.cgi>).  
Genes encoding tRNAs are predicted by tRNAscan-SE  
(Sean Eddy, Washington University School of Medicine, St. Louis,  
<http://genome.wustl.edu/eddy/tRNAscan-SE/>).  
This sequence may not be the entire insert of this clone. It may be  
shorter because we remove overlaps between neighboring submissions.  
The 5' clone is K9I22 and the 3' clone is MJL14.

## FEATURES

source

Location/Qualifiers

1..83650

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/mol\_type="genomic DNA"

/db\_xref="taxon:3702"

/chromosome="3"

Art Unit: 1638

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contains similarity to CHP-rich zinc finger protein
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TGPFGRITASDVETAAGIAPSKSSIAPPPPPPPVTAKATTTNLPPLLPDSSIVPFTA
MQSAVSKNMIESLSVPTFRVGYPVNTDALDLYEKVKPKGVTMTALLAKAAGMALAQH
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RSKQLQPHEYNSGTFTLSNLGMFGVDRFDAILPPGQGAIMAVGASKPTVVADKDGFFS
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Art Unit: 1638

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CDS 16981. .17979  
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QQAGESKKASFDFDADLQIPEMGCFIGDSFIPNACELDFLLTEENNNQMLDDYCGID  
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HRRRLQVLVEAGPDLLAFETIPNKLEAQACVELLEEKVQIPAWICFTSVGEKAPSG  
ESFEECLEPLNKSNNIYAVGINCAPPQFIENLIRKFAKLTKKAIVVYPNSGEVWDGKA  
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KHARLLHPGVRPSEADPERQRSWRRLERQSDLGDLLSTLQSSFGGDEISNDDGFLFAD  
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CDS complement(join(33961. .34021,34114. .34226,34391. .34482,  
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join(36033. .36150,36243. .36283,36497. .36565,36651. .36707,  
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CDS

Query Match 100.0%; Score 1226; DB 4; Length 83650;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]





Art Unit: 1638

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Db      11989 TAGCATCAATCTCCACCGTCCAATTTATTTAGTTGTTGACAAATATCGACCGTCTAAGTTC 11930
Qy      1141 CACACCGACGGCTATAAGAGTTTCATTATAAATTTTAGCAAAATAAAATCAGCAAATAAT 1200
Db      11929 CACACCGACGGCTATAAGAGTTTCATTATAAATTTTAGCAAAATAAAATCAGCAAATAAT 11870
Qy      1201 TTTTCTTGACTAAGCTTAAACGACG 1226
Db      11869 TTTTCTTGACTAAGCTTAAACGACG 11844
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## APPENDIX B

SCORE Search Results Details for Application 10566201 and Search Result us-10-566-201-1.rqe.

[Score Home Page](#)   [Retrieve Application List](#)   [SCORE System Overview](#)   [SCORE FAQ](#)   [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10566201 and Search Result us-10-566-201-1.rqe.

[Go Back to previous page](#)

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

```
Run on:      October 19, 2006, 02:01:17 ; Search time 6423 Seconds
              (without alignments)
              10284.553 Million cell updates/sec
```

Title: US-10-566-201-1  
Perfect score: 1033  
Sequence: 1 gaattcgtggtatagcgtta.....aaatcaatcactttctctaa 1033

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :      GenEmbl:*
1:  gb_env:*
2:  gb_pat:*
3:  gb_ph:*
4:  gb_pl:*
5:  gb_pr:*
6:  gb_ro:*
7:  gb_sts:*
8:  gb_sy:*
9:  gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
```

Art Unit: 1638

14: gb\_om:\*

15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
	1	1033	100.0	1033	2	CS007928		CS007928	Sequence
	2	1033	100.0	1033	2	CS025769		CS025769	Sequence
c	3	1033	100.0	109180	4	AC064879		AC064879	Arabidops
	4	1033	100.0	121668	4	AC022521		AC022521	Arabidops
	5	144.4	14.0	98461	4	ATT6H20		AL096859	Arabidops
	6	142.6	13.8	100906	4	ATF24G16		AL138647	Arabidops
	7	142.4	13.8	89219	4	ATT6K22		AL031187	Arabidops
	8	142.4	13.8	198715	4	ATCHRIV54		AL161554	Arabidops
c	9	140.6	13.6	99254	4	AC002423		AC002423	Genomic s
	10	140.4	13.6	100867	4	AC008047		AC008047	Genomic s
	11	140.2	13.6	78181	4	AB011477		AB011477	Arabidops
	12	139.6	13.5	102299	4	AC018908		AC018908	Arabidops
c	13	137.2	13.3	84544	4	AB005239		AB005239	Arabidops
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c	15	135	13.1	84872	4	AC006593		AC006593	Arabidops
c	16	134.8	13.0	100815	4	ATF12A12		AL133314	Arabidops
	17	133.8	13.0	199667	4	ATCHRIV37		AL161537	Arabidops
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c	23	130.4	12.6	73009	4	AC007069		AC007069	Arabidops
c	24	130.4	12.6	77483	4	AB028607		AB028607	Arabidops
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c	32	127	12.3	115851	4	AC002505		AC002505	Arabidops
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	43	123.8	12.0	2004	2	AX461295		AX461295	Sequence
	44	123.8	12.0	88149	4	AC006201		AC006201	Arabidops
	45	123.8	12.0	103889	4	ATT24C20		AL096856	Arabidops

Art Unit: 1638

## ALIGNMENTS

## RESULT 3

AC064879/c

LOCUS AC064879 109180 bp DNA linear PLN 19-AUG-2000

DEFINITION Arabidopsis thaliana chromosome I BAC T6A9 genomic sequence,  
complete sequence.

ACCESSION AC064879

VERSION AC064879.3 GI:7958959

KEYWORDS HTG.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 109180)

AUTHORS Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,  
Altafi,H., Nguyen,M., Lam,B., Southwick,A., Miranda,M., Brooks,S.,  
Buehler,E., Chao,Q., Chin,C., Chiou,J., Choi,E., Gonzalez,A.,  
Howng,B., Johnson-Hopson,C., Khan,S., Kim,C., Koo,T., Lee,J.M.,  
Lenz,C., Liu,A., Liu,S., Mukharsky,N., Pham,P., Sakano,H.,  
Shinn,P., Toriumi,M., Vaysberg,M., Yu,G., Ecker,J., Theologis,A.  
and Davis,R.W.

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 109180)

AUTHORS Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,  
Altafi,H., Nguyen,M., Lam,B., Southwick,A., Bei,Q., Buehler,E.,  
Chin,C., Chiou,J., Choi,E., Dunn,P., Gonzalez,A., Howng,B., Kim,C.,  
Koo,T., Lee,J.M., Lenz,C., Li,J., Liu,A., Liu,K., Liu,S.,  
Mukharsky,N., Pham,P., Sakano,H., Schwartz,J., Shinn,P.,  
Thaveri,A., Toriumi,M., Vaysberg,M., Walker,M., Yu,G., Ecker,J.,  
Theologis,A. and Davis,R.W.

TITLE Direct Submission

JOURNAL Submitted (24-APR-2000) DNA Sequencing and Technology Center,  
Stanford University, 855 California Avenue, Palo Alto, CA 94304,  
USA

REFERENCE 3 (bases 1 to 109180)

AUTHORS Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,  
Altafi,H., Nguyen,M., Lam,B., Southwick,A., Bei,Q., Buehler,E.,  
Chin,C., Chiou,J., Choi,E., Dunn,P., Gonzalez,A., Howng,B., Kim,C.,  
Koo,T., Lee,J.M., Lenz,C., Li,J., Liu,A., Liu,K., Liu,S.,  
Mukharsky,N., Pham,P., Sakano,H., Schwartz,J., Shinn,P.,  
Thaveri,A., Toriumi,M., Vaysberg,M., Walker,M., Yu,G., Ecker,J.,  
Theologis,A. and Davis,R.W.

TITLE Direct Submission

JOURNAL Submitted (20-MAY-2000) DNA Sequencing and Technology Center,  
Stanford University, 855 California Avenue, Palo Alto, CA 94304,  
USA

REFERENCE 4 (bases 1 to 109180)

AUTHORS Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,  
Altafi,H., Nguyen,M., Lam,B., Southwick,A., Ecker,J., Theologis,A.  
and Davis,R.W.

TITLE Direct Submission

JOURNAL Submitted (19-AUG-2000) DNA Sequencing and Technology Center,

Art Unit: 1638

Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA

COMMENT On May 20, 2000 this sequence version replaced gi:7922104. Bases 1-51,564 of clone T6A9 overlap with bases 55,373-106,937 of BAC clone T7I23 (gb|U89959) and bases 91,185-109,180 overlap with 103,674-121,668 of BAC clone T14P4 (gb|AC022521).

FEATURES

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misc_feature	1. .51564 /note="overlap with bases 55,373-106,937 of BAC clone T7I23 (gb U89959), see Genbank entry for BAC clone T7I23 for annotation in this region."
gene	complement(53259..55668) /gene="T6A9.1"
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Art Unit: 1638

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Query Match 100.0%; Score 1033; DB 4; Length 109180;  
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